

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 18, 2002, 04:48:39 ; Search time 42.56 Seconds

(without alignments)
327.515 Million cell updates/sec

Title: US-09-719-748-2

Perfect score: 1846
Sequence: 1 MEPEKQKQKVEDFYDIGELG.....TEEDIAKKALHPPRRSSTS 360

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SWISSProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1293	70.0	1431	DAKP_HUMAN	P53355 homo sapien
2	703.5	38.1	1176	KMLS_BOVIN	Q28824 bos taurus
3	698	37.8	1914	KMLS_HUMAN	Q15746 homo sapien
4	694	37.6	1147	KMLS_RABIT	P29294 oryctolagus
5	685.5	37.1	1906	KMLS_CHICK	P11799 gallus gall
6	668.5	36.2	414	SI7A_HUMAN	Q9ues5 homo sapien
7	659.5	35.7	397	SI7A_RABIT	Q9gm70 oryctolagus
8	641.5	34.8	372	SI7B_HUMAN	Q94768 homo sapien
9	637	34.5	438	KMLS_SHEEP	O02827 ovis aries
10	605	32.8	607	KMLS_RABIT	P07313 oryctolagus
11	604	32.7	609	KMLS_RAT	P20689 rattus norv
12	545.5	29.6	295	KMLC_DICDI	P25323 dictyostell
13	532	28.8	474	KCC4_RAT	P13334 rattus norv
14	530.5	28.7	370	KCC1_HUMAN	Q14012 homo sapien
15	530.5	28.7	374	KCC1_RAT	Q63450 rattus norv
16	530	28.7	473	KCC4_HUMAN	Q16566 homo sapien
17	528.5	28.6	499	KCCD_HUMAN	Q13557 homo sapien
18	527.5	28.6	466	KCC4_MOUSE	P08414 mus musculu
19	526.5	28.5	533	KCCD_RAT	P15791 rattus norv
20	512	27.7	3038	TRIO_HUMAN	O75962 homo sapien
21	502	27.2	527	KCCG_RAT	P11730 rattus norv
22	493	26.7	424	KPSH_HUMAN	P11801 homo sapien
23	490.5	26.6	533	CDP2_ORYSA	P53683 oryza sativ
24	489.5	26.5	610	CDP1_ARATH	Q06850 arabidopsi
25	487.5	26.4	542	CDP3_ORYSA	P53684 oryza sativ
26	486.5	26.4	740	DKR1_HUMAN	O15075 homo sapien
27	486	26.3	478	KCCA_RAT	P11375 rattus norv
28	486	26.3	756	DKR1_MOUSE	O911m8 mus musculu
29	485.5	26.3	433	DKR1_RAT	O08875 rattus norv
30	482.5	26.1	534	CDP1_ORYSA	P53682 oryza sativ
31	482	26.1	478	KCCA_MOUSE	P11798 mus musculu
32	481	26.1	542	KCCB_MOUSE	P28652 mus musculu
33	478.5	25.9	532	CDPK_DAUCA	P28682 daucus caro

34	478	25.9	542	1	KCCB_RAT	P08413 rattus norv
35	478	25.9	664	1	KCCB_HUMAN	Q13554 homo sapien
36	477.5	25.8	508	1	CDPK_SOYBN	P28583 glycine max
37	476.5	25.8	924	1	CDPK_MOUSE	O70389 mus musculu
38	476	25.8	513	1	CDP2_MAIZE	P49101 zea mays (m
39	475.5	25.8	909	1	CDPK_RAT	O62915 rattus norv
40	475.5	25.8	921	1	CDPK_HUMAN	O14936 homo sapien
41	473.5	25.7	406	1	KPBH_RAT	P31325 rattus norv
42	472.5	25.6	406	1	KPBH_HUMAN	P15755 homo sapien
43	471	25.5	335	1	KCC1_SCHPO	Q9p712 schizosach
44	469.5	25.4	406	1	KPBH_MOUSE	Q9db30 mus musculu
45	465.5	25.2	512	1	K110_ARATH	Q38997 arabidopsi

ALIGNMENTS

```

RESULT 1
ID      DAPK_HUMAN      STANDARD;      PRT;      1431 AA.
AC      P53355;
DT      01-OCT-1996 (Rel. 34, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Death-associated protein kinase 1 (EC 2.7.1.1) (DAP kinase 1).
GN      DAPK1 OR DAPK.
OS      Homo sapiens (human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX      Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE-95129831; PubMed-7828849;
RA      Deiss L.P., Feinstein E., Berissi H., Cohen O., Kimchi A.;
RT      Identification of a novel serine/threonine kinase and a novel 15-kD
RT      protein as potential mediators of the gamma interferon-induced cell
RT      death.
RL      Genes Dev. 9:15-30(1995).
RN      [2]
RP      REVISIONS TO 164-171.
RA      Feinstein E.;
RL      Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
CC      -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC      -1- SIMILARITY: CONTAINS 10 ANK REPEATS.
CC      -1- SIMILARITY: INVOLVED IN MEDIATING INTERFERON-GAMMA-INDUCED CELL
CC      DEATH.
CC      -1- PTM: AUTOPHOSPHORYLATED.
CC      -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC      -1- SIMILARITY: CONTAINS 10 ANK REPEATS.
CC      -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC      -----
CC      THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL; X76104; CAA53712.1; -.
CC      HSSP; Q63450; 1A06.
CC      MIM; 600831; -.
CC      InterPro: IPR002110; ANK.
CC      InterPro: IPR000488; Death.
CC      InterPro: IPR000719; Euk_pkinase.
CC      InterPro: IPR002290; Ser_thr_pkinase.
CC      Pfam; PF00023; ank; 8.
CC      Pfam; PF00531; death; 1.
CC      Pfam; PF00069; pkinase; 1.
CC      SMART; SM00248; ANK; 7.
CC      SMART; SM00005; DEATH; 1.
CC      SMART; SM00220; S_TKC; 1.
CC      PROSITE; PS50088; ANK_REPEAT; 6.
CC      PROSITE; PS50297; ANK_REPEAT_REGION; 1.
CC      PROSITE; PS50017; DEATH_DOMAIN; 1.

```

DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW Transferase; Serine/threonine-protein kinase; Calmodulin-binding;
 KM Phosphorylation; ATP-binding; Repeat; ANK repeat; Apoptosis.
 FT DOMAIN 13
 FT 267 334 CALMODULIN-BINDING.
 FT REPEAT 378 407 ANK 1.
 FT REPEAT 411 440 ANK 2.
 FT REPEAT 444 473 ANK 3.
 FT REPEAT 478 507 ANK 4.
 FT REPEAT 511 540 ANK 5.
 FT REPEAT 544 573 ANK 6.
 FT REPEAT 577 606 ANK 7.
 FT REPEAT 610 639 ANK 8.
 FT REPEAT 876 905 ANK 9.
 FT REPEAT 1163 1197 ANK 10.
 FT DOMAIN 1313 1397 DEATH.
 FT NP_BIND 19 27 ATP (BY SIMILARITY).
 FT BINDING 42 42 ATP (BY SIMILARITY).
 FT ACT_SITE 139 139 BY SIMILARITY.
 FT MUTAGEN 42 42 K->A: LOSS OF ACTIVITY.
 SQ SEQUENCE 1431 AA; 160017 MW; 9EB84811004A155B CRC64;

Query Match 70.0%; Score 1293; DB 1; Length 1431;
 Best Local Similarity 68.2%; Pred. No. 4.3e-71;

Matches 242; Conservative 62; Mismatches 43; Indels 8; Gaps 2;

QY 1 MEFFKQKQKEDFDGEELGSGGFAIVKCKREKSTGLEAFAKFIKKQSRASRGVSRRE 60
 1 MTFKQKQKEDFDGEELGSGGFAIVKCKREKSTGLEAFAKFIKKQSRASRGVSRRE 60
 DB 1 MTFKQKQKEDFDGEELGSGGFAIVKCKREKSTGLEAFAKFIKKQSRASRGVSRRE 60
 QY 61 IEREVSILRQVHNHYITLHDYENRFDVHILEVSGGELDFLQAKSLSEETSTI 120
 61 IEREVSILRQVHNHYITLHDYENRFDVHILEVSGGELDFLQAKSLSEETSTI 120
 DB 61 IEREVSILRQVHNHYITLHDYENRFDVHILEVSGGELDFLQAKSLSEETSTI 120
 QY 121 KQILDGNYVHTKKIAHFQDLKPEINIMLDKNIPRIPIKILDFGLAHEIDEGVEFKNIFGT 180
 121 KQILDGNYVHTKKIAHFQDLKPEINIMLDKNIPRIPIKILDFGLAHEIDEGVEFKNIFGT 180
 DB 121 KQILDGNYVHTKKIAHFQDLKPEINIMLDKNIPRIPIKILDFGLAHEIDEGVEFKNIFGT 180
 QY 181 PEFVAPETVVEPLGLEADWMSIGVITYILLGASPLDGTQKQETLANITSYDDEER 240
 181 PEFVAPETVVEPLGLEADWMSIGVITYILLGASPLDGTQKQETLANITSYDDEER 240
 DB 181 PEFVAPETVVEPLGLEADWMSIGVITYILLGASPLDGTQKQETLANITSYDDEER 240
 QY 241 FSHSTSELAQDFIRKLIVKTRKRLTIOEARHPWTPVDNQOAMVRESVYNLENFRKOY 300
 241 FSHSTSELAQDFIRKLIVKTRKRLTIOEARHPWTPVDNQOAMVRESVYNLENFRKOY 300
 DB 241 FSHSTSELAQDFIRKLIVKTRKRLTIOEARHPWTPVDNQOAMVRESVYNLENFRKOY 300
 QY 301 VRRRWKLSFVSICNHLTSLMKKVVH--RPDEDLRNCSSTDEEDIAARRKALH 352
 301 VRRRWKLSFVSICNHLTSLMKKVVH--RPDEDLRNCSSTDEEDIAARRKALH 352
 DB 301 VRRRWKLSFVSICNHLTSLMKKVVH--RPDEDLRNCSSTDEEDIAARRKALH 352
 RESULT 2
 ID KMLS_BOVIN STANDARD; PRT: 1176 AA.
 AC Q28824;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Myosin light chain kinase, smooth muscle (BC 2.7.1.117) (MCK)
 GN [Contains: Telokin].
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP TISSUE=Stomach;
 RC MEDLINE=93203148; PubMed=1284247;

RA Kobayashi H., Inoue A., Mikawa T., Kuwayama H., Hotta Y., Masaki T.,
 RA Ebashi S.;
 RT "Isolation of cDNA for bovine stomach 155 kDa protein exhibiting
 RT myosin light chain kinase activity.";
 RL J. Biochem. 112:786-791(1992).
 CC -1- FUNCTION: CALCIUM/CALMODULIN-DEPENDENT ENZYME RESPONSIBLE FOR
 CC IN THE N-TERMINUS OF MYOSIN LIGHT CHAINS (MLC), AN EVENT THAT
 CC FACILITATES MYOSIN INTERACTION WITH ACTIN FILAMENTS.
 CC -1- CATALYTIC ACTIVITY: ATP + [myosin light-chain] -> ADP + [myosin
 CC light-chain] phosphate.
 CC -1- SUBUNIT: TELOKIN BINDS CALMODULIN.
 CC -1- ALTERNATIVE PRODUCTS: AT LEAST 3 ISOFORMS OF MCK ARE PRODUCED BY
 CC ALTERNATIVE INITIATION, A NON-MUSCLE FORM (WHICH IS THE LONGEST
 CC FORM), A SMOOTH-MUSCLE FORM AND TELOKIN (A C-TERMINAL SECTION WITH
 CC NO CATALYTIC ACTIVITY).
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
 CC -----
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: S57131; AAB25794.1; -.
 CC HSSP: P56276; ITLK.
 DR InterPro: IPR000719; Euk_Pkinase.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003598; Ig_C2.
 DR InterPro: IPR003600; Ig_Like.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR Pfam: PF00041; fn3; 1.
 DR Pfam: PF00047; Ig; 2.
 DR Pfam: PF00069; pkinase; 1.
 DR SMART: SM00060; FN3; 1.
 DR SMART: SM00410; Ig_Like; 1.
 DR SMART: SM00408; IgC2; 2.
 DR SMART: SM00220; S_TKc; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 KW Transferase; Serine/threonine-protein kinase; Calmodulin-binding;
 KW ATP-binding; Phosphorylation; Immunoglobulin domain; Repeat;
 KW Alternative Initiation.
 FT CHAIN 1 1176
 FT INIT_MET 1022 1176
 FT DOMAIN 100 1022
 FT REPEAT 100 111
 FT REPEAT 112 123
 FT REPEAT 124 135
 FT REPEAT 136 147
 FT REPEAT 148 159
 FT REPEAT 160 171
 FT REPEAT 172 183
 FT REPEAT 184 195
 FT REPEAT 196 207
 FT REPEAT 208 219
 FT REPEAT 220 231
 FT REPEAT 232 243
 FT REPEAT 244 255
 FT REPEAT 256 267
 FT REPEAT 268 279
 FT REPEAT 280 291
 FT REPEAT 292 303
 FT DOMAIN 725 980
 FT DOMAIN 972 1035

Query Match	Best Local Similarity	Matches	Score	DB 1:	Length	1914:	
146:	Conservative	66:	Mismatches	117:	Indels	22:	Gaps
QY	6	OOKVEDFYDGEELSGEFOAIVKCKREKSTGLEVAKFTKROSRASRGVSHRETEREV	65	1510			
DB	1457	EQAVSPFYDIEELSGSKRGQVRLVEKTKRWAKKFKVYSAK-----EKENIROET	1510				
QY	66	SILROYLHNVTTLHDVYENRNDVHILBELVSGGEFLFDLQAK-E-SLSEEARSPFKOLI	124				
DB	1511	SIWNCJLHNFYLCVQVAFEEKANIVVLELVSGGELFERLIDDELTETKECKIKIRQIS	1570				
QY	125	DGVNVLHTKRIAEFDLKPENIMLDKNIPRIKILDFGLAHEIEDGVFEKNIFGPEFY	184				
DB	1571	EGEVLHYKQGVTLHDLKPENIMCVNKT--GTRIKLIDFGARLENAVSLKVLFGPEFY	1628				
QY	185	APETVNEPRLGLBADMWSIGVITYLLISGASPELGDTKOETLANITSVSDPDEEFSHT	244				
DB	1629	APETVNEPFGVATDMWSIGVICYIIVSGISPEPMGDNDNETLANVTSATWDFDEAFDEI	1688				
QY	245	SELAQDRIKRLVKEPFRKLTIOEALHPMT--PPVNDQOAMVRRESVYVNLNENFRKQVRR	303				
DB	1689	SDDKDKITSLKDKMKNRLDCDQCLDHPMLMDTKMEEA-----KTLSDRMKKYMAR	1743				
QY	304	RWKLSEFIVSLCNHLTRSLM-----KVVHLRPDEDLRNCSESTEDDIAR	347				
DB	1744	KWQKTGNVAVRILGRILSSMAMISGLSGRKSSTGSPESPLNAEKLSEBDSQ	1794				
RESULT	4						
KMLS_RABIT	STANDARD;	PRT:	1147	AA.			
AC	P29294; Q28729;						
DC	01-DEC-1992 (Rel. 24, Created)						
DT	15-JUL-1998 (Rel. 36, Last sequence update)						
DE	16-OCT-2001 (Rel. 40, Last annotation update)						
DE	Myosin light chain kinase (EC 2.7.1.117) (MLCK)						
DE	[Contains: Telokin].						
GN	MYLK.						
OS	Oryctolagus cuniculus (Rabbit).						
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.						
OX	NBI_TaxID=9986;						
RN	(1)						
RP	SEQUENCE FROM N.A.						
RC	TISSUE=Smooth muscle;						
RX	MEDLINE=92084694; PubMed=1748666;						
RA	Wolfe P.J., Herring B.P., Griffin S.A., Stull J.T.;						
RT	Molecular characterization of a mammalian smooth muscle myosin light						
RL	chain kinase..;						
RN	J. Biol. Chem. 266:23936-23944(1991).						
	[2]						

RP	SEQUENCE OF 993-1147 FROM N.A. (TELOKIN).	
RA	MEDLINE-92084695; PubMed-1748667;	
RA	Gallagher P.J., Herring B.P.:	
RT	"The carboxyl terminus of the smooth muscle myosin light chain kinase	
RT	is expressed as an independent protein, telokin."	
RL	J. Biol. Chem. 266:23945-23952(1991).	
CC	-1- FUNCTION: PHOSPHORYLATES A SPECIFIC SERINE IN THE N-TERMINUS OF A	
CC	MUSCIN LIGHT CHAIN.	
CC	-1- CATALYTIC ACTIVITY: ATP + [myosin light-chain] - ADP + [myosin	
CC	light-chain] phosphate.	
CC	-1- ALTERNATIVE PRODUCTS: AT LEAST THREE ISOFORMS OF MLCK ARE PRODUCED	
CC	BY ALTERNATIVE INITIATION. A NON-MUSCLE FORM (WHICH IS THE LONGEST	
CC	FORM); A SMOOTH-MUSCLE FORM AND TELOKIN (A C-TERMINAL SECTION WITH	
CC	NO CATALYTIC ACTIVITY).	
CC	-1- DOMAIN: TELOKIN BINDS CALMODULIN.	
CC	-1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.	
CC	-1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.	
CC	THIS SWISS-PROT entry is copyright. It is produced through a collaboration	
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -	
CC	the European Bioinformatics Institute. There are no restrictions on lists	
CC	use by non-profit institutions as long as its content is in no way	
CC	modified and this statement is not removed. Usage by and for commercial	
CC	entities requires a license agreement (See http://www.isb.ch/announce/1sb.ch).	
CC	or send an email to license@1sb.ch).	
CC	-----	
DR	EMBL: M76233; AAA73093.1; -	
DR	EMBL: M76234; AAA31408.1; -	
DR	EMBL: M76181; AAA31409.1; -	
DR	PIR: A41675; A41675.	
DR	HSSP: P56276; 1TLK.	
DR	InterPro: IPR000719; Euk_Pkinase.	
DR	InterPro: IPR003961; FN_III.	
DR	InterPro: IPR003006; Ig_MHC.	
DR	InterPro: IPR003598; Ig_C2.	
DR	InterPro: IPR003600; Ig_Like.	
DR	InterPro: IPR002290; Ser_thr_Pkinase.	
DR	Pfam: PF00047; Ig; 2.	
DR	Pfam: PF00047; Ig; 2.	
DR	Pfam: PF00069; Pkinase; 1.	
DR	SMART: SM00060; FN3; 1.	
DR	SMART: SM00410; IG_1like; 1.	
DR	SMART: SM00408; IGC2; 2.	
DR	SMART: SM00220; S_TKC; 1.	
DR	PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.	
DR	PROSITE: PS00108; PROTEIN_KINASE_ST; 1.	
DR	PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.	
KW	Transferase: Serine/threonine-protein kinase; Calmodulin-binding;	
KW	ATP-binding; Phosphorylation; Immunoglobulin domain; Repeat;	
KW	Alternative initiation.	
FT	CHAIN	1 1147
FT	MYOSIN LIGHT CHAIN KINASE, SMOOTH-MUSCLE	
FT	ISOYME.	
FT	TELOKIN.	
FT	INIT_MET	993 993
FT	DOMAIN	100 288
FT	REPEAT	100 111
FT	REPEAT	112 123
FT	REPEAT	124 132
FT	REPEAT	133 144
FT	REPEAT	145 156
FT	REPEAT	157 168
FT	REPEAT	169 180
FT	REPEAT	181 192
FT	REPEAT	193 204
FT	REPEAT	205 216
FT	REPEAT	217 228
FT	REPEAT	229 240
FT	REPEAT	241 252
FT	REPEAT	253 264
FT	REPEAT	265 276
FT	REPEAT	277 288
FT	DOMAIN	574 644
FT	FIBRONECTIN TYPE-III.	

Query Match 37.6%, Score 694; DB 1; Length 1147;
Best Local Similarity 41.6%, Pred. No. 6,5e-35;
Matches 146; Conservative 63; Mismatches 120; Indels 22; Gaps 6;

```

FT DOMAIN 696 951 PROTEIN KINASE.
FT DOMAIN 943 1006 CALMODULIN-BINDING.
FT DOMAIN 1056 1123 IG-LIKE C2-TYPE DOMAIN.
FT NP_BIND 702 710 ATP (BY SIMILARITY).
FT BINDING 725 725 ATP (BY SIMILARITY).
FT ACT_SITE 817 817 BY SIMILARITY.
FT DOMAIN 1138 1147 POLY-GLU.
FT CONFLICT 1114 1114 C->R (IN REF. 2).
FT SEQUENCE 1147 AA; 125719 MM; F039E624CGE31024 CRC64;

QY 6 QQQVEDFYDIBEGSGGQFAIVYKCKREKSTGLEVAAKTKKRSQASRRGVSRREIEREV 65
Db :||| ||||| ||||| : : : : : : : : : : : : : : : : : : : : : : : : :
QY 689 EOKVSDPFDIERLEGSGFGQVFRVLEKRTKGITMGKFFKVASAK-----EKENIPAEI 742
Db :||| ||||| ||||| : : : : : : : : : : : : : : : : : : : : : : : : :
QY 66 SILRQVLLHHNYITLTDVYENRFDVYHILELVSGGLPFPLOAKE-SLSEEAFTSPIKOLL 124
Db :||| ||||| ||||| : : : : : : : : : : : : : : : : : : : : : : : : :
QY 743 GIMNCILHPRKVLQCCDAEEKANIYMLVEIYSGGLFERIIDDELFELRECIKIMROIS 802
Db :||| ||||| ||||| : : : : : : : : : : : : : : : : : : : : : : : : :
QY 125 DGVNVLTKTKIAHFDLKPENIMLDKNIPRIPIKILDEGLAHLEIDGVEFKNIGTPEFV 184
Db :||| ||||| ||||| : : : : : : : : : : : : : : : : : : : : : : : : :
QY 803 EGVEYIKHGGIVHLDLKPENIMCVNKT--GPIRIKILDFGLARLRLENAGSLKVLFTPEFV 860
Db :||| ||||| ||||| : : : : : : : : : : : : : : : : : : : : : : : : :
QY 185 APEIVNPEPLGLEADNMSIGVITVITLLSGASPLGDTQOETLANITSVSYDDEEFESHT 244
Db :||| ||||| ||||| : : : : : : : : : : : : : : : : : : : : : : : : :
QY 245 SELAKDFRKLKLVETRRRLITQEALRPWIT-TPVDNCOAWRRSVNLENFRKQYVR 303
Db :||| ||||| ||||| : : : : : : : : : : : : : : : : : : : : : : : : :
QY 921 SDAKDFISNLTKKMKRKRRLDOCTQLGHPMLKKDKPKNMEA-----KTSIDKMKKYYMAR 975
Db :||| ||||| ||||| : : : : : : : : : : : : : : : : : : : : : : : : :
QY 304 RKKLSFSTVSLCNIHLTRSLM-----KKVHLRPEDIRNCESDTEEDDIAR 347
Db :||| ||||| ||||| : : : : : : : : : : : : : : : : : : : : : : : : :
QY 976 KWQKTGNVRAIRIGRLSNAMISGLSGRRKSSPGSPSPPLTAERLFEEDVSO 1026
Db :||| ||||| ||||| : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 5
KMLS_CHICK STANDARD: PRI: 1906 AA.
AC P11799; P19038;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Myosin light chain kinase, smooth muscle and non-muscle isoymes
DE (EC 2.7.1.117) (MCK) [Contains: Telokin].
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxId=9031;
NN [1]
RP SEQUENCE FROM N.A. (MCK-210)
RX MEDLINE=96033976; Pubmed=7589469;
RA Waterson D.M., Collinge M., Lukes T.J., van Eldik L.J., Bitukov K.G.,
RA Stepanova O.V., Shirinsky V.P.;
RT "Multiple gene products are produced from a novel protein kinase
RT transcription region.";
RL FEBS Lett. 373:217-220(1995).
NN [2]
RP SEQUENCE FROM N.A. (MCK-108)
RX MEDLINE=90192792; Pubmed=2315320;
RA Olson N.J., Pearson R.B., Needleman D.S., Hurwitz M.J., Kemp B.E.,
RA Means A.R.;
RT "Regulatory and structural motifs of chicken gizzard myosin light
RT chain kinase.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:2284-2288(1990).
NN [3]
RP SEQUENCE OF 649-1906 FROM N.A., AND PARTIAL SEQUENCE.
NC TISSUE=Fibroblast;
```


[illegible]

[illegible]

RP [1]
 RN SEQUENCE FROM N.A..
 RX MEDLINE=96139839; PubMed=8569750;
 RA Pato M.D., Kerc E., Lye S.J.;
 RT "Phosphorylation and partial sequence of pregnant sheep myometrium
 RT myosin light chain kinase."
 RL Mol. Cell. Biochem. 149:59-65(1995).
 CC -1- FUNCTION: PHOSPHORYLATES A SPECIFIC SERINE IN THE N-TERMINUS OF A
 CC MYOSIN LIGHT CHAIN.
 CC -1- CATALYTIC ACTIVITY: ATP + [myosin light-chain] - ADP + [myosin
 CC light-chain] phosphate.
 CC -1- DOMAIN: TELOKIN BINDS CALMODULIN.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

DR	EMBL; S80867; AAB50715.2; -	
DR	HSSP; P56276; ITLK.	
DR	InterPro; IPR000719; Euk_pkinase.	
DR	InterPro; IPR003006; Ig_MHC.	
DR	InterPro; IPR003598; Ig_c2.	
DR	InterPro; IPR002290; Ser_thr_pkinase.	
DR	Pfam; PF00047; Ig_1.	
DR	Pfam; PF00069; pkinase_1.	
DR	SMART; SM00408; IGC2; 1.	
DR	SMART; SM00220; S_TKC; 1.	
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; PARTIAL.	
DR	PROSITE; PS00108; PROTEIN_KINASE_ST; 1.	
DR	PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.	
KW	Transferase; Serine/threonine-protein kinase; Calmodulin-binding;	
KW	ATP-binding; Phosphorylation; Immunoglobulin domain.	
FT	NON_TER	1
FT	DOMAIN	<1 241
FT	DOMAIN	233 296
FT	DOMAIN	346 413
FT	BINDING	15 15
FT	ACT_SITE	107 107
FT	DOMAIN	283 438
FT	DOMAIN	433 438
QO	SEQUENCE	438 AA; 49503 MW; 77A02F4885A10B51 CRC64; POLY-GLU.

[illegible]

```
QY      324 -KKVHLRPDEDLNCESDTEEDIR 347
          | | | : : : | : :
Db      292 RKSSTGSPSPINAKELESEEDVSQ 316
```

RESULT	10
KMLC_10	
ID	KMLC_RABBIT
STANDARD:	PRT: 607 AA.
AC	P07313;
DT	01-APR-1988 (Rel. 07, Created)
DT	01-APR-1990 (Rel. 14, Last sequence update)
DT	16-OCT-2001 (Rel. 40, Last annotation update)
DE	Myosin light chain kinase, skeletal muscle (EC 2.7.1.117) (MLCK).
OS	Oryctolagus cuniculus (Rabbit).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX	NCBI_TaxID=9986;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	MEDLINE=90110242; Pubmed=1686558;
RT	Herring B.P., Stull J.T., Gallagher P.J.;
RL	"Domain characterization of rabbit skeletal muscle myosin light chain
RL	kinase.";
RL	J. Biol. Chem. 265:1724-1730(1990).
RN	[2]
RP	SEQUENCE OF 1-603.
RX	MEDLINE=87101105; Pubmed=3542042;
RA	Takio K., Blumenthal D.K., Walsh K.A., Titani K., Krebs E.G.;
RT	"Amino acid sequence of rabbit skeletal muscle myosin light chain
RT	kinase.";
RL	Biochemistry 25:8049-8057(1986).
RN	[3]
RP	SEQUENCE OF 295-603.
RA	MEDLINE=86104095; Pubmed=3841288;
RA	Takio K., Blumenthal D.K., Edelman A.M., Walsh K.A., Krebs E.G.,
RA	Titani K.;
RT	"Amino acid sequence of an active fragment of rabbit skeletal muscle
RT	myosin light chain kinase.";
RL	Biochemistry 24:6028-6037(1985).
RN	[4]
RP	STRUCTURE BY NMR OF 577-602.
RX	MEDLINE=92263094; Pubmed=1585175;
RA	Ikuira M., Clore G.M., Gronenborn A.M., Zhu G., Klee C.B., Box A.;
RT	"Solution structure of a calmodulin-target peptide complex by
RT	multidimensional NMR.";
RL	Science 256:632-638(1992).
CC	-1- FUNCTION: PHOSPHORYLATES A SPECIFIC SERINE IN THE N-TERMINUS OF A
CC	CYSAN LIGHT CHAIN.
CC	-1- CATALYTIC ACTIVITY: ATP + [myosin light-chain] = ADP + [myosin
CC	light-chain] phosphate.
CC	-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC	the European Bioinformatics Institute. There are no restrictions on its
CC	use by non-profit institutions as long as its content is in no way
CC	modified and this statement is not removed. Usage by and for commercial
CC	entities requires a license agreement (See http://www.isb.ch/announce/
CC	or send an email to license@isb.sib.ch).
CC	-----
DR	EMBL; J05194; AAA31400.1; -
DR	PIR; A25830; A25830.
DR	PIR; A05120; A05120.
DR	PIR; A35021; A35021.
DR	PDB; 2BBW; 31-JAN-94.
DR	PDB; 2BNM; 31-JAN-94.
DR	InterPro; IPR000719; Euk_pkinase.
DR	InterPro; IPR002290; Ser_thr_pkinase.
DR	Pfam; PF00069; pkinase; 1.
DR	SMART; SMO0220; S_TKC; 1.
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR	PROSITE; PS00106; PROTEIN_KINASE_ST; 1.
DR	PROSITE; PSS0011; PROTEIN_KINASE_DOM; 1.

Transferase; Serine/threonine-protein kinase; Calmodulin-binding;
 KW ATP-binding; Phosphorylation; Acetylation; 3D-structure;
 FT INIT_MET 0
 FT MOD_RES 1
 FT DOMAIN 296 551
 FT DOMAIN 585 597
 FT NP_BIND 302 310
 FT BINDING 325 325
 FT ACT_SITE 417 417
 FT CONFLICT 335 335
 FT HELIX 581 595
 FT TURN 596
 SQ SEQUENCE 607 AA; 65337 MW; 66677641751A04C8 CRC64;
 Query Match 32.8%; Score 605; DB 1; Length 607;
 Best Local Similarity 40.4%; Pred. No. 7.7e-30;
 Matches 124; Conservative 63; Mismatches 106; Indels 14; Gaps 5;
 OY 17 EELSGQFAIVKCKREKSTGLEAYAKFKKRSRSGVSEELEREYSILROYLHNHV 76
 DB 300 EALGGKFGAVCTCERSTGLKLAQKVIKQTPK-----DKEMVLELEVNNQLNHRNL 353
 OY 77 ITHDYENRTDVNHLLEYSGSELPFLAOK-SESEATSFIKOILDGVNYLHTKKI 135
 DB 354 IQLYALIEPHETVLEMEYIEGSELPFLAOK-SESEATSFIKOILDGVNYLHTKKI 413
 OY 136 AHFDLKPENIMLDKNIPPIPHIKLIDGLAHEIDEGVEKKNFGPEFAPEIYVNEPGL 195
 DB 414 LHLDPENILCVNTGHL--VKIIDGLARRYPNEKLVNGPEFSPPEVYVNDQIS 471
 OY 196 LEADMSIGITYIILSGASPFGLDGTKEPLANTSVSYDFDEEFSHTSELAQDFIRKL 255
 DB 472 DKTDMSLGVITYMLLSGLSPFLGDDDTFLNNVLSANNYFDETEFAVSDKAKDFVSNL 531
 OY 256 LVETRRRLTIQALRHPWITPVNDQNAVRR--ESVNLNFRKQYVRRKLSIYS 313
 DB 532 IVKQGRMSAOCALHPWLNLAERAKRCNRRLKSOILL--KKYLMKRRMKNEIYVS 588
 OY 314 LCNHLTR 320
 DB 589 AANRFK 595
 RESULT 11
 KMLC_RAT STANDARD; PRT; 609 AA.
 AC P20689;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Myosin light chain kinase, skeletal muscle (EC 2.7.1.117) (MCK).
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 CC NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88273159; PubMed=2839493;
 RA Roush C.L., Kennelly P.J., Glaccum M.B., Helfman D.M., Scott J.D.,
 RA Krebs E.G.;
 RT "Isolation of the cDNA encoding rat skeletal muscle myosin light
 RT chain kinase. Sequence and tissue distribution."
 RL J. Biol. Chem. 263:10510-10516(1988).
 CC -1- FUNCTION: PHOSPHORYLATES A SPECIFIC SERINE IN THE N-TERMINUS OF A
 CC MYOSIN LIGHT CHAIN.
 CC -1- CATALYTIC ACTIVITY: ATP + [myosin light-chain] = ADP + [myosin
 CC -1- light-chain] phosphate.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its

use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; J03886; AAA41625.1; ALT_SEQ.
 DR PIR: A28798; A28798.
 DR HSP: P00518; 1PK.
 DR InterPro: IPR002290; Ser_thr_kinase.
 DR InterPro: IPR002290; Ser_thr_kinase.
 DR Pfam: PF00069; PKinase; 1.
 DR SMART: SM00220; S_TKc; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 KW Transferase; Serine/threonine-protein kinase; Calmodulin-binding;
 KW ATP-binding; Phosphorylation; Acetylation.
 FT INIT_MET 0
 FT MOD_RES 1
 FT DOMAIN 298 553
 FT DOMAIN 587 599
 FT NP_BIND 304 312
 FT BINDING 327 327
 FT ACT_SITE 419 419
 SQ SEQUENCE 609 AA; 65685 MW; 0073A22659BD1358 CRC64;
 Query Match 32.7%; Score 604; DB 1; Length 609;
 Best Local Similarity 39.1%; Pred. No. 8.9e-30;
 Matches 120; Conservative 67; Mismatches 106; Indels 14; Gaps 5;
 OY 17 EELSGQFAIVKCKREKSTGLEAYAKFKKRSRSGVSEELEREYSILROYLHNHV 76
 DB 302 EALGGKFGAVCTCERSTGLKLAQKVIKQTPK-----DKEMVLELEVNNQLNHRNL 355
 OY 77 ITHDYENRTDVNHLLEYSGSELPFLAOK-SESEATSFIKOILDGVNYLHTKKI 135
 DB 356 IQLYALIEPHETVLEMEYIEGSELPFLAOK-SESEATSFIKOILDGVNYLHTKKI 415
 OY 136 AHFDLKPENIMLDKNIPPIPHIKLIDGLAHEIDEGVEKKNFGPEFAPEIYVNEPGL 195
 DB 416 LHLDPENILCVNTGHL--VKIIDGLARRYPNEKLVNGPEFSPPEVYVNDQIS 473
 OY 196 LEADMSIGITYIILSGASPFGLDGTKEPLANTSVSYDFDEEFSHTSELAQDFIRKL 255
 DB 474 DKTDMSLGVITYMLLSGLSPFLGDDDTFLNNVLSANNYFDETEFAVSDKAKDFVSNL 533
 OY 256 LVETRRRLTIQALRHPWITPVNDQNAVRR--ESVNLNFRKQYVRRKLSIYS 313
 DB 534 ITRQGRMSAOCALHPWLNLAERAKRCNRRLKSOILL--KKYLMKRRMKNEIYVS 590
 OY 314 LCNHLTR 320
 DB 591 AANRFK 597
 RESULT 12
 KMLC_DICDI STANDARD; PRT; 295 AA.
 AC P25323;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Myosin light chain kinase (EC 2.7.1.117) (MCK).
 GN MKA.
 OS Dictyostelium discoideum (Slime mold).
 CC Eukaryota; Mycetozoa; Dictyostellida; Dictyostellum.
 CC NCBI_TaxID=44689;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=AX3;
 RX MEDLINE=9134075; PubMed=1651931;
 RA Tan J.L., Spudich J.A.;

RT "Characterization and bacterial expression of the Dictyostelium
RT myosin light chain kinase cDNA. Identification of an autoinhibitory
RT domain.";
RL J. Biol. Chem. 266:16044-16049(1991).
RN [2]
RP REVISIONS.
RA Spudich J.A.;
RL Submitted (Aug-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP PARTIAL SEQUENCE.
RC STRAIN-AX3;
RX MEDLINE=90337997; PubMed=2380188;
RT Tan J.L.; Spudich J.A.;
RT "Dictyostelium myosin light chain kinase. Purification and
RT characterization.";
RL J. Biol. Chem. 265:13818-13824(1990).
CC -1- FUNCTION: PHOSPHORYLATES A SPECIFIC SERINE IN THE N-TERMINUS OF A
CC MYOSIN LIGHT CHAIN.
CC -1- CATALYTIC ACTIVITY: ATP + [myosin light-chain] = ADP + [myosin
CC light-chain] phosphate.
CC -1- ENZYME REGULATION: POSSESSES AN AUTOINHIBITORY DOMAIN.
CC AUTOPHOSPHORYLATION APPEARS TO INCREASE THE ENZYMATIC ACTIVITY.
CC DOES NOT HAVE A CALMODULIN-BINDING DOMAIN.
CC SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CAMK SUBFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M64176; AAB06337.1; -;
DR PIR: A40811; A40811.
DR PIR: A37125; A37125.
DR HSP: 063450; 1A06.
DR DictyDB: DD01034; mlka.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
KW transferase; Serine/threonine-protein kinase; ATP-binding;
KW phosphorylation.
FT DOMAIN 8 265 PROTEIN KINASE.
FT DOMAIN 264 295 AUTOINHIBITORY DOMAIN.
FT NF_BIND 14 22 ATP (BY SIMILARITY).
FT BINDING 37 37 ATP (BY SIMILARITY).
FT ACT_SITE 130 130 BY SIMILARITY.
SQ SEQUENCE 295 AA; 33406 MW; 546CAEDB8F6ECD0B CRC64;

Query Match 29.6%; Score 545.5; DB 1; Length 295;
Best Local Similarity 40.1%; Pred. No. 1.3e-26;
Matches 123; Conservative 50; Mismatches 119; Indels 15; Gaps 5;

OY 8 KVEDFDIGELSGGQFAIYKCKREKSTGLEAYAKFFIKKRSRARGVSRREE-IEREVS 66
DB 3 EKEKIVYEFKEELGSGAFSIYVLEGNKQTKQRYAKIVK-----SELGKDYENKMLKMEVD 57
OY 67 ILROVLHNNVITLHDVYENRTDVVHILEVSGELDFPLAOKESLSEEAATSPYKQILDG 126
DB 58 ILKVNHPNIIALKLELDFPEKTLVLMELVTGELFPKIVYEGSGYSADAANLVKTIYSA 117
OY 127 VNVLTFTKKIAHFOLKRPENIMLDKNIRPIHKLIDELGLAHIEGCVFEKNTFCPEVPAP 186
DB 118 VGLHAGNIVYHRDLKPRNLLKSKENHL-EVALADFGLSKIGTGLVQWTRACGSPSYVAP 176
OY 187 EIVNVEPLGLEADWMSIGVITYILLGASPLGDTKQETLANITVSVDPEDEFFSHTSE 246

DB 177 EVLNATGYDKDEVDMWSIGVITYILLGCPPEYGDTPVEIFRQINMEANYEPPEEYWGIGSK 236
OY 247 LAKDFIRKLKLVKTRKRLTIOELRHFWITVDNOQAMVRESVYNLENFKQVRRRWK 306
DB 237 EAKDFIGKLLVDVSKRLNATNALNHPWLKSNNSNNTI-----DTVKM----KEYIVEROK 288
OY 307 LSFSTVS 313
DB 289 TOTKLVN 295

RESULT 13
ID KCCL4_RAT STANDARD; PRT; 474 AA.
AC P13234;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Calcium/calmodulin-dependent protein kinase type IV catalytic chain
DE (EC 2.7.1.123) (CAM kinase-GR) (CAM IV) [Contains: Calsperrmin].
GN CAMK4.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RN SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=91288548; PubMed=1648230;
RA Omlstede C. A., Bland M.M., Merrill B.M., Sahyoun N.;
RT "Relationship of genes encoding Ca2+/calmodulin-dependent protein
RT kinase Gr and calsperrmin: a gene within a gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:5784-5788(1991).
RN [2]
RN SEQUENCE FROM N.A.
RX MEDLINE=91304387; PubMed=1649385;
RA Means A.R., Cruzalegui F., Lemagneresse B., Needleman D.S.,
RA Slaughter G.R., Ono T.;
RT "A novel Ca2+/calmodulin-dependent protein kinase and a male germ
RT cell-specific calmodulin-binding protein are derived from the same
RT gene.";
RL Mol. Cell. Biol. 11:3960-3971(1991).
RN [3]
RN SEQUENCE OF 250-474 FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY; TISSUE-Brain;
RX MEDLINE=89174647; PubMed=2538431;
RA Omlstede C. A., Jensen K.F., Sahyoun N.;
RT "Ca2+/calmodulin-dependent protein kinase enriched in cerebellar
RT granule cells. Identification of a novel neuronal
RT calmodulin-dependent protein kinase.";
RL J. Biol. Chem. 264:5866-5875(1989).
RN [4]
RN SEQUENCE OF 306-474 FROM N.A., AND SEQUENCE OF 335-361.
RC STRAIN-SPRAGUE-DAWLEY;
RX MEDLINE=89123272; PubMed=2914893;
RA Ono T., Slaughter G.R., Cook R.G., Means A.R.;
RT "Molecular cloning sequence and distribution of rat calsperrmin, a
RT high affinity calmodulin-binding protein.";
RL J. Biol. Chem. 264:2081-2087(1989).
CC -1- FUNCTION: CAM KINASE GR IS A NEURONAL-SPECIFIC PROTEIN KINASE,
CC ENRICHED IN CEREBELLAR GRANULE CELLS.
CC -1- FUNCTION: CALSPERRMIN IS A HEAT-STABLE, ACIDIC, CALMODULIN-BINDING
CC PROTEIN.
CC -1- CATALYTIC ACTIVITY: ATP + protein = ADP + O-phosphoprotein.
CC -1- ALTERNATIVE PRODUCTS: CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE
CC TYPE IV CATALYTIC CHAIN AND CALSPERRMIN ARE OBTAINED BY ALTERNATIVE
CC SPLICING.
CC -1- TISSUE SPECIFICITY: CALSPERRMIN IS PREDOMINANTLY FOUND IN MAMMALIAN
CC TESTIS AND BRAIN.
CC -1- PWM: THE N-TERMINAL OF CALSPERRMIN IS BLOCKED.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CAMK SUBFAMILY.
CC -----

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

EMBL: M63334; AAA40865.1; ALU_SEQ.
EMBL: M74488; AAA40856.1; -
EMBL: M64757; AAA40857.1; -
EMBL: J04600; AAA41867.1; -
EMBL: J04446; AAA40990.1; -
PIR: A41103; TVRCA.
HSP: P00518; 1PK.
InterPro: IPR000719; Euk_pkinase.
InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR Transferrase: Serine/threonine-protein kinase; ATP-binding; Calmodulin-binding; Testis; Alternative splicing.
KW CHAIN 306
FT DOMAIN 42 296
FT NP_BIND 48 56
FT BINDING 71 71
FT ACT_SITE 160 160
FT DOMAIN 318 337
FT DOMAIN 393 399
FT DOMAIN 403 413
FT DOMAIN 372 372
FT CONFLICT 474 AA; 53133 MM; 56F71AC564DED23 CRC64;
SEQUENCE

Query Match 28.8%; Score 532; DB 1; Length 474;
Best Local Similarity 36.8%; Pred. No. 1.5e-25;
Matches 119; Conservative 62; Mismatches 112; Indels 30; Gaps 7;

QY 5 KQKVEDFDYDGEELSGGFAYVKKCRKSTGLEAAFKIKKRSRASRGVSRREIRE 64
DB 34 KRPLSDFEVESELGATSIYRKQKGTQKPYALKVTKT-----VKKIIVTE 85
QY 65 VSILROYLHNVTLLHDVYENRTDVVHILVSGGLDFPLAOKSLSSEATSFIRK 124
DB 86 IGVLLRISHPIIKLKEIFETPEISLVLELTGGLDFRIVEKGYSDRADAVKQIL 145
QY 125 DGVNLTHTKTAHFDLKPENIMLDKNIPHP--IKLIDFGLAHEIEDGVEFRKNIFG 182
DB 146 EAVAYLHNGIVHNDLKPENLVA---TPAPDAFLKADGSLKIVEHQVLMKTVGTEG 202
QY 163 FVAPETVYEPFLGADMSIGVITYLLSGAPFL---GDTQOELTANTSVSYDDEE 239
DB 203 YCAPELLGCAVGPEDVMASGIIITYLLLCFEPFYDERGD--QFMFRLLNCEYFISF 260
QY 240 FFSHSELAKPIRKTLVKEFRKRLTIOELRHFWITPVNDQAMVRESVNLNFRKQ 299
DB 261 WNDVSLNKLKDLVLPDKRLTTPQALQHPWVG-----KAANFVHMDTQAK 312
QY 300 Y---VRRMKLSFISVLCNHL 318
DB 313 LQEFNARKLKAAYKAVVASRL 335

RESULT 14
KCL_HUMAN STANDARD: PRT; 370 AA.
AC 014012;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Calcium/calmodulin-dependent protein kinase type I (EC 2.7.1.123)
DB (CAM kinase I).
OS CAMK1.
GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;

RP SEQUENCE FROM N.A. Pubmed=7641687;
RA Haribabu B., Hook S.S., Selbert M.A., Goldstein E.G., Tomhave E.D.,
RA Edelman A.M., Snyderman R., Means A.R.;
RT "Human calcium-calmodulin dependent protein kinase I: cDNA cloning,
RT domain structure and activation by phosphorylation at threonine-177
RT by calcium-calmodulin dependent protein kinase I kinase.";
RL EMBL J. 14.3679-3686(1995).
CC -1- FUNCTION: PHOSPHORYLATES SYNAPSIN I.
CC -1- CATALYTIC ACTIVITY: ATP + protein = ADP + O-phosphoprotein.
CC -1- ENZYME REGULATION: ACTIVATED BY CA++/CALMODULIN. MUST BE
CC -1- PHOSPHORYLATED TO BE MAXIMALLY ACTIVE.
CC -1- SUBUNIT: MONOMER.
CC -1- TISSUE SPECIFICITY: UBIQUITOUS.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CAMK SUBFAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

EMBL: L41816; AAA99458.1; -
DR HSP: Q63450; 1A06.
DR MIM: 604998; -
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR Transferrase: Serine/threonine-protein kinase; Calmodulin-binding;
KW Phosphorylation; ATP-binding; Alternative splicing.
KW Phosphorylation; ATP-binding; Alternative splicing.
FT DOMAIN 20 276
FT NP_BIND 26 34
FT BINDING 49 49
FT ACT_SITE 141 141
FT MOD_RES 177 177
FT MUTAGEN 49 49
SEQUENCE 370 AA; 41337 MM; 57FA20BCED0FA76C CRC64;

Query Match 28.7%; Score 530.5; DB 1; Length 370;
Best Local Similarity 35.7%; Pred. No. 1.4e-25;
Matches 120; Conservative 65; Mismatches 126; Indels 25; Gaps 9;

QY 4 KQKVEDFDYDGEELSGGFAYVKKCRKSTGLEAAFKIKKRSRASRGVSRREIRE 62
DB 10 WKQADRIDYDFRDVLTGAFSEVILAEKRTKLVAINCIK-ELAEKEG-----SME 64
QY 63 REVSLROYLHNVTLLHDVYENRTDVVHILVSGGLDFPLAOKSLSSEATSFIRK 122
DB 65 NEIAYLHKIKHNIVAYADIDYESGCHLVLMQVSGGLDFRIVEKGYTERDASRLIFQ 124
QY 123 ILDGVNLTHTKTAHFDLKPENIML--LDKNIPHPKILIDFGLAHEIEDGVEFRKNIFG 180
DB 125 VLDAYKTLHDLDIVHNDLKPENLTVSLDED--SKMISDFGLSKMDEPSCVSTACGT 181
QY 181 PEFVAPETVYEPFLGADMSIGVITYLLSGAPFLGDTQOELTANTSVSYDDEEF 240

Sat May 18 15:09:09 2002

us-09-719-748-2.rsp

Page 14

.....